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Draft Genome Sequence of *Photobacterium halotolerans* S2753, Producer of Bioactive Secondary Metabolites

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We report here the whole draft genome sequence of marine isolate *Photobacterium halotolerans* S2753, which produces the known antibiotic holomycin and also ngercheumicins and solonomides A and B, which interfere with virulence of methicillin-resistant *Staphylococcus aureus* strains by interacting with the quorum-sensing system.

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Photobacterium halotolerans strain S2753 is a Gram-negative marine bacterium that was isolated from a mussel during the Danish global expedition Galathea 3 (1). It is able to inhibit the growth of both Gram-positive and Gram-negative pathogens such as *Staphylococcus aureus* (human pathogen) and *Vibrio anguillarum* (fish pathogen) (1, 2). This specific strain has been shown to produce a variety of secondary metabolites with distinct bioactivities (3, 4). It produces holomycin, a known antibiotic (2), as well as a series of ngercheumicin analogues (5) (K. Adachi, Y. Kawabata, H. Kasai, M. Katsuta, and Y. Shizuri, 13 September 2007, Japanese patent application JP 2007-230911 A) and most interestingly two novel cyclodepsipeptides named solonomide A and solonomide B (3, 4).

Antimicrobial resistance in pathogens is a serious problem derived both from the rapid adaptation of microorganisms to antimicrobials and the recent stagnancy in antibiotic discovery. *S. aureus* is a versatile pathogen that has caused particular concern recently due to fast antimicrobial resistance development among both clinical and community isolates (6–8). Therefore, therapeutics that do not exert a killing effect, but rather interfere with virulence of the organism, e.g., by interfering with the quorum-sensing systems, have been studied and developed in recent years (9). *P. halotolerans* S2753 produces compounds capable of reducing the expression of virulence in *S. aureus* (10). Both the ngercheumicins and solonomides interfere with the Agr system of *S. aureus*, with solonomide B having the strongest interaction (10). Also, this compound can compete with the four classes of autoinducing peptides (AIPs) in *S. aureus*, although interference with AIP class III is weak.

This announcement reports the draft genome sequence of *P. halotolerans* S2753, a strain producing chemical compounds with interesting features for application in biotechnological and medical fields.

High-purity genomic DNA was extracted by successive phenol:chloroform:isoamyl-alcohol purification steps followed by precipitation with isopropanol, treatment with RNase, and final purification and precipitation steps (11). Quantification was done in

1% agarose gel electrophoresis using a NanoDrop spectrometer (Saveen Werner, Sweden) and Qubit 2.0 analyzer (Invitrogen, United Kingdom).

The sequencing of the genomes was performed by the Beijing Genomic Institute (Shenzhen, China). Libraries of 500 bp were used for 100-bp paired-end sequencing of genomes using Illumina sequencing technology on an HiSeq2000 with a minimum coverage of 100. This generated 5.03 million reads of clean data, making a total of 462,754,934 bases. The data were assembled into 82 contigs (>200 bp) covering 4,533,138 bases by *de novo* assembly in CLC Genomic Workbench, version 7 (CLC Bio, Aarhus, Denmark).

In order to predict clusters involved in secondary metabolite synthesis, the reported genome was run on the analysis pipeline antiSMASH (12,13), revealing the potential of this specific strain. Besides the holomycin cluster, 11 other putative clusters encoding secondary metabolites were identified in the *P. halotolerans* S2753 genome.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JMIB00000000](https://www.ncbi.nlm.nih.gov/nuclseq/JMIB00000000). The version described in this paper is version JMIB01000000.

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This is Galathea 3 contribution no. p106.

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